

Figure 1A

1 GTTGACTCATTTGCTGTTGAACCTTACTGTCAACAGCACTGTAACCTCATGCCTGAGCCAAGC 60
 61 TTGTCTAACACGTATATTTTCTCTGTAAAGCACATCACAGCCTTTCTGCACCTTAGGAACA 120
 121 TTAGACAGCACTTCAGCAGTACACTTGGGGGCCATTTTAAACAATTAAATCACTGATAGG 180
 181 CTCGCTCCGCTCAGGGGGGCCCCAGACAGGGTTTCCCATGGCAGCACCCAGGCACGCC 240
 241 CGGCGCACCTGCTGCCCCGAACCCCTGGCTCCAGGGGGCAATGAGGGGGCAGTGAAGGG 300
 301 GCACTACTCCTCGGGCATTGCCTAGAGAAGCGAGACCGTCCCGCCCTCCCGCTGGCCCTC 360
 361 CTTCTCTCCCGCCCGGGGCCGCGCAATTCTCCGCAGAGGGACAGTGGGCTCATATGT 420
 1 M L 2
 421 TAAGACCTCTGATCACTAGATCCCTGCATCTCCACTGAACAACCAAGGCACCCCTACTC 480
 3 R P L I T R S P A S P L N N Q G T P T P 22
 481 CGGCACAACCTCACAAATCCAATGCGCATGCCACACTGATGTGGGCAGCCACATGTACA 540
 23 A Q L T K S N A H V H T D V G S H M Y T 42
 541 CCAGCAGCCTGGCCACCCCTACCAAATACCTGTATCCAGAATCAGAAGACTTTGTGATG 600
 43 S S L A T L T K Y P V S R I R R L C D G 62
 601 GTACAGAGCCCATAGTTTGGACAGTCTCAAACAGCACTATTCACTGACAGAGATGGAC 660
 63 T E P I V L D S L K Q H Y F T D R D G Q 82
 661 AGATGTTGAGATATATCTTGAATTTTCTACGAACATCCAACCTCCTCATCTTGTGATG 720
 83 M F R Y I L N F L R T S K L L I L D D F 102
 721 TCAAGGACTACACTTTGTTATATGAAGAGGCAAAATATTTTCAGCTTCAGCCCATGTTGT 780
 103 K D Y T L L Y E E A K Y F O L Q P M L L 122
 781 TGGAGATGGAAGATGGAAGCAGGACAGAGAACTGGTCGCTTTTCAAGGCCCTGTGAGT 840
 123 E M E R W K O D R E T G R F S R P C E C 142
 841 GCCTGTTTGTGTGGCCCCAGACCTCAGAGAAAGGATCACGCTAAGTGGTGACAAATCCT 900
 143 L V C V A P D L R E R I T L S G D K S L 162
 901 TGGTAGAAGAGTGTTTCCAGAGATCGGCGATGTGATGTGCAACTTTTACAGTGCAGGCT 960
 163 V E E V F P E I G D V M C N F I S A G W 182

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Figure 1B

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961  GGAATCATGACTCCACGCACATCGTCAGGTTTCCACTAAGTGGCTACTGTCACTCAACT 1020
183  N H D S T H I V R F P L S G Y C H L N S 202

1021 CAGTCCAGGTCTCTCGAGAGGTTGCAGCAAAGAGGATTTGAAATCGTGGGCTCCTGTAGGG 1080
203  V Q V L E R L Q Q R G F E I V G S C R G 222

1081 GAGGAGTGGGCTCATCCTAGTTCAGCAAATACGTCCTTCATAGGGAACCTGAGGCGGATGC 1140
223  G V G S S 227

1141 CCTCCCCTACCTCCATCATCTCTGGATAAAGCAAGAGCCTCTGGACTAAACGGACATATTT 1200

1201 CTTATGCAAAAAGGAAAACACACACAACCTAATAAACAAATAATAAAAAAGGGACATTTGT 1260

1261 GTGCAGTTGGGACAGAAAACCAAGTCCTGCACCTAAAAATTGAATAAAGATGCATTTATA 1320

1321 TGCAATAGAGACCACACCTGTATTTCATATGGGAACAATTGGAATAGTTCACTCAAAAAAA 1380

1381 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1418

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Figure 2

| | | | | |
|----------|-------|--|--|--------------|
| | | 1 | | 50 |
| K+betaM3 | (1) | ----- | | ----- |
| MECHP-2 | (1) | ----- | | ----- |
| KCNMB1 | (1) | ----- | | ----- |
| CG10465 | (1) | ----- | | ----- |
| CG10440 | (1) | MDRERERDVKALEPRDLSSSTGRIYARSDIKISSSPTVSPYISNSSSPPT | | |
| | | 51 | | 100 |
| K+betaM3 | (1) | -----MLRSLITRSPSPINNQ----- | | -----SITTEAQ |
| MECHP-2 | (1) | -----MSRSLITRSPSPINNQ----- | | -----SITTEAQ |
| KCNMB1 | (1) | ----- | | ----- |
| CG10465 | (1) | -----MSESISGSD----- | | -----HKILL |
| CG10440 | (51) | PPASSSVTPFGLFGAVAAAFVGGASSAGASSYLHGNHKPTITETCVAA | | |
| | | 101 | | 150 |
| K+betaM3 | (25) | LIRSNHVTVDVGGHVTSSLATLTKYFVSRTRRLCDTEPIVLDLSLKH | | |
| MECHP-2 | (25) | LIRSNHVTVDVGGHVTSSLATLTKYFVSRTRRLCDTEPIVLDLSLKH | | |
| KCNMB1 | (1) | -----SVKKLVMAQKRETRRLCLGVTMVCAITYYILVITVLPYQ | | |
| CG10465 | (14) | KKSSOYLHVTVDVGGHVTSSLATLTKYFVSRTRRLCDTEPIVLDLSLKH | | |
| CG10440 | (101) | ASRYTTPFVVDVGGHVTSSLATLTKYFVSRTRRLCDTEPIVLDLSLKH | | |
| | | 151 | | 200 |
| K+betaM3 | (75) | YFIDRDGNFRMLNLFNRSSLLILDFPKYTLLEPAKYRQIQPMILEM | | |
| MECHP-2 | (75) | YFIDRDGNFRMLNLFNRSSLLILDFPKYTLLEPAKYRQIQPMILEM | | |
| KCNMB1 | (44) | KSMWTDESKMLLENNRDRCEIKGRVPEYPCFVNVSAAGRWAHTYHT | | |
| CG10465 | (63) | ITLIRCCNHEGILNLFNRSSLLILDFPKYTLLEPAKYRQIQPMILEM | | |
| CG10440 | (151) | YFIDRDGNFRMLNLFNRSSLLILDFPKYTLLEPAKYRQIQPMILEM | | |
| | | 201 | | 250 |
| K+betaM3 | (125) | ERWQDRETG-----RFSRPECCTVC----- | | |
| MECHP-2 | (125) | ERWQDRETG-----RFSRPECCTVVR----- | | |
| KCNMB1 | (94) | ETTDENQQC-----S----- | | |
| CG10465 | (113) | ERALYHQEPKPICRIPITSQ---KEEQLLSVSLKPAVILVQRQNNKY | | |
| CG10440 | (201) | ESMKDRVRNGNYLVAPPTPPARHIKTSRPTSASPECNYVVALH---- | | |
| | | 251 | | 300 |
| K+betaM3 | (146) | -----VAPDIRERITLSDK-----LVEEVEFF | | |
| MECHP-2 | (147) | -----VAPDIRITLSDK-----LVEEVEFF | | |
| KCNMB1 | (105) | -----YVGGNDYQDARDEVK-----DAKAEQ | | |
| CG10465 | (161) | SYTSTDDNLLKNIELFDKILRNERLLEIKVIGSPETCCWSYGHGK | | |
| CG10440 | (246) | -----VAPDIRITLSDK-----LVEEVEFF | | |
| | | 301 | | 350 |
| K+betaM3 | (169) | ELGEMVNFIS-RCWH-----ESTHVRFPPLGYCHLNSVOVIERIQ | | |
| MECHP-2 | (170) | ELGEMVNFIS-RCWH-----ESTHVRFPPLGYCHLNSVOVIERIQ | | |
| KCNMB1 | (129) | QQVFYCFEAP---R-GNE-----AVLVRFLRYDQQLFESFWPTFLIT | | |
| CG10465 | (211) | KVALVCCSTVYATDRKHKTKEVFHARTYLELVLLEARNAPDQILIC | | |
| CG10440 | (269) | ELGEMVNFIS-RCWH-----ESTHVRFPPLGYCHLNSVOVIERIQ | | |
| | | 351 | | 395 |
| K+betaM3 | (212) | RGEPILVSCRGCVGS----- | | |
| MECHP-2 | (213) | RGEPILVSCRGCVGS----- | | |
| KCNMB1 | (170) | RGELITAMVK-----GLSLIAAQ----- | | |
| CG10465 | (261) | ATSSARVSSRGTSIIVYSDDEEEETGLARLRNSKNRNNPS----- | | |
| CG10440 | (314) | RGEPILVSCRGCVGS----- | | |

Figure 3



